



# Modeling historical fecal coliform loadings to large European rivers and resulting in-stream concentrations



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## ABSTRACT

Information on fecal coliform (FC) concentrations in European rivers is scarce. The objective of this study was to identify hotspots of water pollution in Europe and provide information on the different FC sources and their contributions to the loads that lead to concentrations in rivers. Model simulations were carried-out with the large-scale water quality model WorldQual to assess the calculated loads regarding to its associated sources and to further estimate the related in-stream concentration. For the year 1995, model results indicated that FC loadings were higher in central Europe with 500 to above 2000  $10^{10}$  cfu  $\text{km}^{-2} \text{a}^{-1}$  than in northern and eastern Europe where loadings ranged between 0 and 200  $10^{10}$  cfu  $\text{km}^{-2} \text{a}^{-1}$ . Major sources of FC loadings are domestic sewage, followed by scattered settlements (private treatment), urban surface runoff and manure application. Concentrations showed similar regional patterns as loadings, with high concentrations in central Europe and low concentrations in northern and eastern Europe.

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## 1. Introduction

Bacteria in surface waters are the most common source to cause gastrointestinal infections like diarrhea, typhoid, etc. (Okoh et al., 2007). Fecal coliform (FC) bacteria are frequently used or implemented as an indicator for pathogen organisms, e.g. in Europe, FC bacteria are considered as an indicator in the European Community Bathing Water Directive (76/160/EEC) (European Commission, 1975), the United States Environmental Protection Agency (USEPA) consider FC as an indicator for recreation waters (USEPA, 1986; USEPA, 2012) and in the World Health Organization (WHO) FC are used as indicator in the guidelines on the use of wastewaters in agriculture and aquaculture (WHO, 1989). The use of indicators was introduced more than a century ago and was very effective in reducing the number of outbreaks of pathogen diseases especially typhoid and cholera, but even though a significant number of outbreaks still occurs (NRC, 2004). The application of indicators has frequently been questioned because of their ability to predict pathogenic microorganisms (Ahmed et al., 2008). An indicator should have similar intrinsic properties and responses to environmental variations as the pathogen, which it is supposed to represent. But coliform bacteria survival rates are shorter than those of

pathogenic viruses and protozoa, furthermore, the transport of viruses features a different characteristic than coliform transport. Therefore, the presence of coliforms is a sign of fecal contamination, whereas the absence of coliforms does not ensure that the water is free of other pathogens (NRC, 2004; Wu et al., 2011).

Instead of indicator bacteria new molecular biology techniques can be used. Molecular methods can increase the detection limit and decrease detection time. Enteroviruses and bacteriophages may also be alternative indicators of gastroenteritis illness but there are more studies required to validate their adequacy (Ahmed et al., 2008; NRC, 2004). It is assumed that in the future a combination of the new molecular methods and/or alternative indicators and fecal indicator bacteria will provide valuable information (Ahmed et al., 2008; Wu et al., 2011). This results from the conclusion that a single indicator or a small set of indicators is not able to represent all classes of waterborne diseases which endanger human health (NRC, 2004; Wu et al., 2011).

Sampling of microbial contamination is very costly and time consuming (Anderson and Davidson, 1997). Therefore, comprehensive assessments of fecal contamination in rivers are rarely carried-out. Few data is available from authorities, for example the Water Information System for Europe (WISE), does not provide information on fecal contamination of rivers apart from the Bathing Water Quality Status, which is a combined indicator comprising FC and other factors/substances such as pH, color and ammonia. A common way to expand the knowledge on a specific topic is to

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apply models, which can be used to identify hotspots, i.e. regions with high in-stream concentrations or loadings and to characterize the source of a pollutant (Benham et al., 2006).

Large-scale models of water pollution are less common than watershed or field scale models. A single large-scale pathogen modeling approach is known to the authors, which was made by Hofstra et al. (2013) who calculated Cryptosporidium loadings on a 0.5° resolution worldwide. For other pollutants such as nutrients several large-scale models exist which also focus on the calculation of loadings (Behrendt et al., 2002; Green et al., 2004; Grizzetti and Bouraoui, 2006; Seitzinger et al., 2002). The only large-scale modeling approaches to calculate nutrient in-stream concentrations was carried out by Arheimer et al. (2012) with the BALTic Sea basin Hydrological Predictions for the Environment (Balt-HYPE) and with WorldQual (Malve et al., 2012; Reder et al., 2013; Voß et al., 2012; Williams et al., 2012).

Other pathogen modeling exercises have been performed on the small or catchment scales. In Table A.1 several pathogen models are presented. This includes models on fecal coliforms, *E. coli*, Campylobacter, Cryptosporidium and Giardia. All of these pathogens are released from fecal material. Additionally, information is given on the models linked to the pathogen model and if diffuse and/or point sources were considered. Pathogen models are linked to other models, most commonly to hydrology models, to ensure that transport within the river and from land to rivers is adequately represented.

Most pathogen models mentioned in Table A.1 distinguish between point and diffuse sources as potential input pathways for pathogens into the environment. Point sources are sewage treatment plants, storm water overflow (Desai et al., 2011; Wilkinson et al., 1995), direct discharges from agriculture (e.g. drainage systems) (Tian et al., 2002; Wilkinson et al., 1995), leaks from onsite-sewage facilities (Desai et al., 2011), and meat processing plants (Tian et al., 2002). The diffuse source with the greatest impact on diffuse loadings is manure (applied as fertilizer or from grazing animals). Dorner (2004) and Sadeghi and Arnold (2002) further differentiate into tillage incorporation of manure and manure applied straight to the surface. Ferguson et al. (2007) and Collins and Rutherford (2004) estimate the loads from direct fecal deposition into streams, Walker and Stedinger (1999) differentiate into age classes of the animals (cattle) to capture loading differences in the excreted manure. Sadeghi and Arnold (2002) and Collins and Rutherford (2004) consider the effects of bufferstrips and Sadeghi and Arnold (2002) additionally distinguish between soluble and adsorbed bacteria. Furthermore, other studies account for wildlife such as birds and beavers which contribute to the diffuse loadings (Cho et al., 2012; Desai et al., 2011).

Some pathogen models consider either point or diffuse sources. Medema and Schijven (2001) focus on point sources from sewage treatment plants other models simply calculate the in-stream concentration from diffuse loadings, e.g. from livestock (Jenkins et al., 1984; Fraser et al., 1998; Haydon and Deletic, 2006). Fraser et al. (1998) applies a regression function to calculate the in-stream concentration. Further models based on a regression function have also been applied by Crowther et al. (2003), Eleria and Vogel (2005) and Lawrence (2012).

Microorganisms are either directly discharged from point sources into rivers or are released from land areas due to precipitation. Via precipitation the pathogens reach the river by surface runoff or by infiltration into the soil and transport through interflow and groundwater (Dorner, 2004; Haydon and Deletic, 2006; Hofstra et al., 2013; Servais et al., 2007; Wilkinson et al., 1995). After pathogens are released, the change of in-stream concentrations can be estimated by a first order decay process that is described by Chick's law (Crane and Moore, 1986). Here, the decay

is a function of die-off, sedimentation (Ouattara et al., 2013; Wilkinson et al., 1995), pH dependencies, predation (Wilkinson et al., 1995), and solar radiation (on soil and in water) (Cho et al., 2012; Tian et al., 2002; Wilkinson et al., 1995).

The objective of this study is to identify the major sources of FC reaching rivers and indicating patterns of FC loadings and in-stream concentrations. This is achieved by implementing the relevant transport and decay and loss processes of FC in the large-scale water quality model WorldQual (Malve et al., 2012; Voß et al., 2012; Williams et al., 2012). Herein the different approaches found in literature were evaluated with regards to their applicability for large-scale modeling. The evaluation was conducted considering the three criteria a water quality model has to fulfill as established by Jamieson et al. (2004): i) to characterize and track microbial sources, ii) to model the survival and transport of microorganisms within/on the landscape, and iii) to model the survival and transport of microorganisms in streams and lakes.

Large-scale models assist in identifying the water quality status over large areas; hence fill gaps in spatial and temporal observations (Voß et al., 2012). This leads to the identification of key regions (hotspot areas), with high pollutant in-stream concentrations, within a hydrological boundary (Oliver et al., 2009). A large-scale assessment is performed to set priorities and rank areas in terms of pollution to others. The model results can assist in general political decisions and information and are not aimed to be used for individual watershed management strategies, thus a down-scaling is not intended. The scope of the paper is to identify hotspot areas; hence a sensitivity and uncertainty analysis are unfortunately out of the reach of this paper. But such an analysis will be fruitful and is therefore an objective for further research.

The regional focus of our analysis is the European continent, because of accessible input data that are easily available and presumably more accurate than in other parts of the world such as Africa or Asia. From our literature review it turned out that even in Europe recent datasets of measurements are scarce. Therefore, historic FC values from the years 1990–1995 were chosen to validate the model as the most comprehensive set of measurements was available for this time period (GEMStat, 2012).

## 2. Methods

The large-scale water quality model WorldQual is embedded within the modeling framework WaterGAP3 (Fig. B.1) and linked to the hydrology model (Alcamo et al., 2003; Schneider et al., 2011; Verzano, 2009) and water use models (aus der Beek et al., 2010; Flörke et al., 2013). WorldQual was already successfully tested on the European scale for biochemical oxygen demand (BOD<sub>5</sub>), total nitrogen (TN), total phosphorus (TP), and total dissolved solids (TDS) (Malve et al., 2012; Reder et al., 2013; Voß et al., 2012; Williams et al., 2012).

WorldQual is a large-scale water quality model that provides results in form of loadings and in-stream concentrations. The model operates on a 5 by 5 arc-minute grid resolution on a monthly basis. Loadings are calculated separately for point sources and diffuse sources. Point sources include domestic sewage, wastewater from manufacturing industries, and urban surface runoff (Williams et al., 2012). Diffuse sources comprise agricultural inputs and geogenic background loadings (Malve et al., 2012). Additionally, scattered settlements are considered and contribute to both types of sources. A detailed description of the calculation of the loadings is given in Section 2.1.

Once loadings are appointed to each grid cell, the load is divided by the river discharge of the grid cell in order to calculate in-stream concentrations (Voß et al., 2012). Furthermore, the substance-specific and temperature dependent decay takes place. This is described in more detail in Section 2.2. Finally, grid cell in-stream concentrations are routed towards the river mouth following a high-resolution drainage direction map (schematic representation Fig. B.2) (Lehner et al., 2008). The hydrology model of WaterGAP3 requires precipitation, air temperature and solar radiation as climate input. This input was derived from the Water and Global Change (WATCH) Forcing Data (WFD) for the time period 1958–2001 (Weedon et al., 2011). While the temporal resolution of the climate input is on a daily basis, the spatial resolution of the WFD is 0.5° by 0.5°, which was disaggregated to the 5 arc-minute grid cells. Discharge from manufacturing sectors reaching surface waters (return flows) were simulated by WaterGAP3. Land-cover data required as input for the hydrology module was derived from the CORINE 2000 data base (EEA, 2007) for

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